Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Claim 1. (Currently Amended) A method for detecting specifically an allele of a ~~pharmacologically~~ pharmacogenetically relevant gene involved in drug metabolism in a sample, said allele comprising a target nucleotide sequence that is unique to said allele, said method comprising the steps of:

(a) contacting ~~the~~ said sample with a nucleic acid probe under differential hybridization conditions that allow said nucleic acid probe to hybridize specifically to a nucleic acid molecule in said sample, wherein said nucleic acid molecule comprises a ~~comprising said~~ target nucleotide sequence, and wherein either said nucleic acid probe or said nucleic acid molecule is labeled with one or more scattered-light detectable particles of a size between 1 and 500 nm inclusive, thereby forming hybridized nucleic acid molecules that are labeled;

(b) illuminating said one or more scattered-light detectable particles bound to said hybridized nucleic acid molecules using non-evanescent wave light under conditions which produce scattered light from said ~~particle~~ one or more scattered-light detectable particles ~~wherein~~ and in which light scattered from ~~one or more said particles~~ said one or more scattered-light detectable particles can be detected by a human eye with less than 500 times magnification and without electronic amplification; and

(c) detecting light scattered by said one or more scattered-light detectable particles under said conditions ~~as a measure of~~ which indicates the presence of said allele in said sample.

Claim 2. (Previously presented): The method of claim 1, further comprising the step of amplifying a portion of said nucleic acid molecule in said sample, and contacting the amplified nucleic acid molecule with said nucleic acid probe.

Claim 3. (Previously presented): The method of claim 1, wherein said nucleic acid probe (i) is not labeled with scattered-light detectable particles and (ii) is a capture probe

that is immobilized on a solid surface, and wherein said nucleic acid molecule comprising said target nucleotide sequence is labeled with scattered-light detectable particles.

Claim 4. (Currently amended): The method of claim 1, further comprising contacting the sample with a capture probe (i) that is immobilized on a solid surface and (ii) that hybridizes to said nucleic acid molecule comprising said target nucleotide sequence, wherein said nucleic acid molecule is ~~which is~~ not labeled with scattered-light detectable particles, and wherein said nucleic acid probe ~~in step (a)~~ is labeled with scattered-light detectable particles.

Claim 5. (Currently amended): The method of claim 3, wherein said ~~step (a) comprises contacting~~ contacting the sample with a nucleic acid probe comprises contacting the sample with a plurality of different nucleic acid probes that differentially hybridize to different alleles of said ~~pharmacologically~~ pharmacogenetically relevant gene involved in drug metabolism.

Claim 6. (Previously presented): The method of claim 5, wherein said plurality of different nucleic acid probes are immobilized at different spots on a solid surface.

Claims 7-8. (Canceled).

Claim 9. (Currently amended): The method of claim 1, further comprising labeling said nucleic acid probe or said nucleic acid ~~molecules~~ molecule that ~~comprise~~ comprises said target nucleotide sequence by incorporating a moiety that provides an attachment site and/or a cleavage site.

Claims 10-58. (Canceled).

Claim 59. (Currently amended): The method of claim 9, wherein said labeling ~~step involves~~ involves polymerase chain reaction, random-prime labeling, nick-translation, biased random-prime labeling, primer extension, extension displacement transcription incorporation, ligase chain reaction, ligation of multiple oligomers amplification, rolling circle amplification, strand displacement amplification, or transcription-mediated amplification.

Claim 60. (Previously presented): The method of claim 9, wherein said incorporated moiety is a modified nucleotide.

Claim 61. (Previously presented): The method of claim 9, wherein said incorporated moiety is a hapten-derivatized nucleotide or bromodeoxyuridine.

Claim 62. (Currently amended): The method of claim 61, wherein said incorporated moiety is a hapten-derivatized nucleotide, and wherein said hapten-derivatized nucleotide is derivatized with biotin, fluorescein, digoxigenin, or dinitrophenol.

Claim 63. (Currently amended): The method of claim 9, wherein said labeling ~~step further~~ further comprises attaching said scattered-light detectable particles to said nucleic acid probe or said nucleic acid molecule comprising said target nucleotide sequence.

Claim 64. (Currently amended): The method of claim 61, wherein said labeling ~~step further~~ further comprises attaching scattered-light detectable particles that are derivatized with anti-hapten antibodies or anti-bromodeoxyuridine antibodies to said nucleic acid probe or said nucleic acid molecule comprising said target nucleotide sequence.

Claim 65. (Currently amended): The method of claim 62, wherein said labeling ~~step further~~ further comprises attaching scattered-light detectable particles that are derivatized with avidin or streptavidin to said nucleic acid probe or said nucleic acid molecule comprising said target nucleotide sequence.

Claim 66. (Currently amended): The method of claim 64, wherein said incorporated moiety is bromodeoxyuridine, and wherein said nucleic acid molecule that comprises said target nucleotide sequence ~~labeled with bromodeoxyuridine~~ are fragmented prior to hybridization with said nucleic acid probe.

Claim 67. (Currently amended): The method of claim 59, wherein said labeling ~~step comprises~~ comprises using one or more primers that is a gene-specific primer or an allele-specific primer.

Claim 68. (Currently amended): The method of claim 4, wherein said ~~step of~~ contacting the sample with a capture probe comprises contacting the sample with a plurality of different capture probes that differentially hybridize to different alleles of said ~~pharmacologically~~ pharmacogenetically relevant gene involved in drug metabolism.

Claim 69. (Currently amended): The method of claim 68, wherein said ~~step of~~ contacting the sample with a capture probe comprises contacting the sample with a plurality of different capture probes that are immobilized at different spots on a solid surface.

Claim 70. (Currently amended) : The method of claim 1, wherein the ~~pharmacologically~~ pharmacogenetically relevant gene involved in drug metabolism encodes a cytochrome P450 protein.

Claim 71. (Currently amended) : The method of claim 1, wherein the ~~pharmacologically~~ pharmacogenetically relevant gene involved in drug metabolism is a member of the CYP2D family.

Claims 72-74. (Canceled).

Amendments to the Drawings:

The four attached replacement sheets replace Figures 6A, 6B, 6C and 6D filed on September 17, 2001. The changes in Figure 6A through to Figure 6D, which include deleting references to SEQ ID NOs., are shown in the four annotated sheets.

Attachment: Four (4) Replacement Sheets containing Figures 6A, 6B, 6C and 6D
Four (4) Annotated Sheets Showing Changes to Figures 6A, 6B, 6C and 6D